

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/583,832  
Source: IFWP  
Date Processed by STIC: 7/10/06

# ***ENTERED***



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/583,832

DATE: 07/10/2006  
TIME: 10:19:54

Input Set : A:\Avalon 271.txt  
Output Set: N:\CRF4\07102006\J583832.raw

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3 <110> APPLICANT: Avalon Pharmaceuticals
5 <120> TITLE OF INVENTION: Prostate-Specific Proteins Expressed in Cancer and
6   Methods of Use Thereof
8 <130> FILE REFERENCE: 689290-271
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/583,832
C--> 11 <141> CURRENT FILING DATE: 2006-06-21
13 <150> PRIOR APPLICATION NUMBER: 60/531,809
14 <151> PRIOR FILING DATE: 2003-12-22
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1567
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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28 actccacca cagctgggag caggtgccgg agccccggcc tgcattggccc tgtgaaggcc      180
29 actctgggcg tttgggtggg cgtgagtgcc ttcctctgct cccagcatgt ggttttctcc      240
30 gttggccgcc tcttgacct cctggtgcct gacatcccag agtctgtgga gatcaaagtg      300
31 aagcgggagt actacctggc taagcaggca ctggctgaga atgaggttct ttttggaaacg      360
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33 acggttccca aggccagcca gctgcagcag tgacgcctgg aaggacatct ggtgggtcctt      480
34 aggggagtg gcccctcctga gccctgcgag cagcgtcctt ttcctcttcc ctgaggcagc      540
35 ggctgtgtga accgctggct gctgttggtc ctcactctctg ggcacattgc ctgcttcccc      600
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38 ccaagggacc ctgtccctcg gtggcctccc caggcccctg gacacgacag ttctcctcag      780
39 gcaggtgggc tttgtggtcc tcgcccggcc tggccacatc gccctctcct cttacacctg      840
40 gtgaccttcg aatgtttcag agcgcagggc cgttctccct cgtgtcctct ggacccaccc      900
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55 <210> SEQ ID NO: 2

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56 <211> LENGTH: 4431
57 <212> TYPE: DNA
58 <213> ORGANISM: Homo sapiens
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63 aggtgggcca tgacctccga gacctcttcc ggaagccact gtgccaggat gctgcggcga      180
64 cggggccagg aagaggacag caccgtcctg atcgatgtga gccccctga ggagagaag      240
65 aggggctctt acgggagcac agcccacgcc tcggagccag gtggacagca agcggccgcc      300
66 tgcagagctg ggagtcctgc caagccccgg atcgacttcg tctcgtttg ggaggaggac      360
67 ctgaagctag acaggcagca ggacagtgcc gcccgggaca gaacagacat gcacaggacc      420
68 tggcgggaga cttttctgga taatcttcgt gcggctgggc tgtgtgtaga ccagcaggac      480
69 gtccaggcac ggaacaccac agtgactac gcctcctca gcgcctcctg ggctgtgctc      540
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71 tccaactggc cggccggcct gctggcatgg ctgggcatcc ccaacgtcct gctggagggt      660
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73 ttcctcggga gtgacaacca ggacaccttc ttcacaagca ccaagaggca ccaaattctg      780
74 tttgagatcc tggccaagac cccgtatggc cagagaaga aaaacctgct tgggatccac      840
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92 taccacacct tgtttggagt ccgcaatgag gagtgcgcgg ctggaggctg cctgatcgag     1920
93 ctggcacagg agctcctggt catcatggtg ggcaagcagg tcatcaacaa catgcaggag     1980
94 gtctctatcc cgaagctaaa gggctggtgg cagaagttcc ggcttcgctc caagaagagg     2040
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102 gccgcgcgcg acaaccgcac gtgcagtgtg gcaggacgag tcgcagacag aactcctcag     2520
103 acaccggatt aaagaaggaa gaggtttttt tattcggccc ggggcgtcgg cagactcgtg     2580
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133 atgaagcttc cctgggctaa cttgctaccc cgcagcaatc ccagtgtggc cgtctgcttg 4380
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137 &lt;210&gt; SEQ ID NO: 3

138 &lt;211&gt; LENGTH: 843

139 &lt;212&gt; TYPE: PRT

140 &lt;213&gt; ORGANISM: Homo sapiens

142 &lt;400&gt; SEQUENCE: 3

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145 1 5 10 15
148 Gly Pro Pro Leu Pro Thr Leu Cys Pro Ala Val Arg Thr Gly Leu Tyr
149 20 25 30
152 Cys Arg Asp Gln Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr
153 35 40 45
156 Ser Ser Gly Ser His Cys Ala Arg Met Leu Arg Arg Arg Ala Gln Glu
157 50 55 60
160 Glu Asp Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys
161 65 70 75 80
164 Arg Gly Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln
165 85 90 95
168 Gln Ala Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Asp
169 100 105 110
172 Phe Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp

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177          130          135          140
180 Phe Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp
181 145          150          155          160
184 Val Gln Asp Gly Asn Thr Thr Val His Tyr Ala Leu Leu Ser Ala Ser
185          165          170          175
188 Trp Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro
189          180          185          190
192 Leu Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu
193          195          200          205
196 Ala Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val
197          210          215          220
200 Pro Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg
201 225          230          235          240
204 Phe Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg
205          245          250          255
208 His Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu
209          260          265          270
212 Lys Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu
213          275          280          285
216 Ser Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu
217          290          295          300
220 Gly Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His
221 305          310          315          320
224 Trp Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val
225          325          330          335
228 Arg Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly
229          340          345          350
232 Phe Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val
233          355          360          365
236 Phe Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu
237          370          375          380
240 Leu Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp
241 385          390          395          400
244 Cys Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly
245          405          410          415
248 Arg Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala
249          420          425          430
252 Leu Trp Ala Val Leu Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr
253          435          440          445
256 Leu Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg
257          450          455          460
260 Pro Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro
261 465          470          475          480
264 Ile Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg
265          485          490          495
268 Arg Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val
269          500          505          510

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273          515          520          525
276 Val Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg
277          530          535          540
280 Ile Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile
281 545          550          555          560
284 Leu Ser Lys Ile Tyr Val Ser Leu Ala His Val Leu Thr Arg Trp Glu
285          565          570          575
288 Met His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe Thr Leu Lys Val
289          580          585          590
292 Phe Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val Tyr Ile Ala
293          595          600          605
296 Phe Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr His Thr Leu
297          610          615          620
300 Phe Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly Cys Leu Ile Glu
301 625          630          635          640
304 Leu Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln Val Ile Asn
305          645          650          655
308 Asn Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp Trp Gln Lys
309          660          665          670
312 Phe Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser Ala Gly Ala
313          675          680          685
316 Ser Gln Gly Pro Trp Glu Asp Tyr Glu Leu Val Pro Cys Glu Gly
317          690          695          700
320 Leu Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe Gly Phe Val Thr
321 705          710          715          720
324 Ile Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe Ala Leu Leu Asn
325          725          730          735
328 Asn Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe Val Cys Glu Tyr
329          740          745          750
332 Arg Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly Ile Trp Phe His
333          755          760          765
336 Ile Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn Ala Phe Leu
337          770          775          780
340 Leu Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr Tyr Arg Trp Thr
341 785          790          795          800
344 Arg Ala His Asp Leu Arg Gly Phe Leu Asn Phe Thr Leu Ala Arg Ala
345          805          810          815
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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date